



SEQUENCE LISTING

<110> ADLER, JON ELLIOT

<120> T2R TASTE RECEPTORS AND GENES ENCODING SAME

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<141> 2001-04-05

<150> 60/195,532

<151> 2000-04-07

<150> 60/247,014

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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 65 70 75 80
 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
 85 90 95
 Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
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 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
 115 120 125
 Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
 130 135 140
 Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
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 Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
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 Asn Asn Asn Thr Arg Leu Asn Trp Gln Ile Lys Asp Leu Asn Leu Phe
 180 185 190
 Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
 195 200 205
 Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
 210 215 220
 Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
 225 230 235 240
 Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
 245 250 255
 Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
 260 265 270
 Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
 275 280 285
 Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
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 Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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 35 40 45
 Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
 50 55 60
 Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
 65 70 75 80
 Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
 85 90 95
 Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
 100 105 110
 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
 115 120 125
 Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
 130 135 140

Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
145 150 155 160

Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
165 170 175

Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
180 185 190

Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
195 200 205

Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
210 215 220

Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
225 230 235 240

Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
245 250 255

Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
260 265 270

Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
275 280 285

Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
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Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
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Leu

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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35 40 45

Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
50 55 60

Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
65 70 75 80

Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
85 90 95

Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
100 105 110

Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
115 120 125

Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
130 135 140

Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu
145 150 155 160

Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
165 170 175

Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
180 185 190

Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
195 200 205

Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
210 215 220

Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
225 230 235 240

Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
245 250 255

Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
 260 265 270

Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 275 280 285

Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
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Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
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Gln Thr Leu

<210> 7
 <211> 930
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175
 Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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 Thr Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu
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 Lys Thr Ser Ser Pro
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<210> 9

<211> 930

<212> DNA

<213> Homo sapiens

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 atctcctcag ctgatcaaat tattgctgct ctggcagtct ccagagttgg tttgctctgg 180

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gtaatattat tacattggtg ttcaactgtg ttgaatccaa cttcatctaa tttaaaagta 240
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<210> 10
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 10

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      20          25          30

Ile Ala Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile
      35          40          45

Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
      50          55          60

His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
      65          70          75          80

Ile Ile Phe Ile Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
      85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
      100          105          110

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
      115          120          125

Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu
      130          135          140

Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Glu Glu Cys Glu Gly
      145          150          155          160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Met His Leu Ser Asn
      165          170          175

Leu Thr Val Ala Met Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
      180          185          190

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Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Ile His
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Ile Leu Leu Ala Ile
225 230 235 240

Tyr Phe Leu Cys Leu Ile Ile Ser Phe Trp Asn Phe Lys Met Arg Pro
245 250 255

Lys Glu Ile Val Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro
260 265 270

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Asn Lys Thr Leu Lys Gln
275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Val Thr Cys Trp Ala Lys Gly Gln
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Asn Gln Ser Thr Pro
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 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60
 Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
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 165 170 175
 Ala Thr Val Thr Thr Leu Gly Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Leu Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Ile Phe Phe Leu Leu Leu Cys Ala Val
 225 230 235 240
 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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 Thr Phe Leu Ser Val Leu Arg Gln Val Arg Tyr Trp Val Lys Gly Glu
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 Lys Pro Ser Ser Pro
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<210> 13
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 Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln Ile Leu
 35 40 45
 Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
 50 55 60
 Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
 65 70 75 80
 Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
 85 90 95
 Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140
 Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255

Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg
 290 295

<210> 15

<211> 900

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 299

<212> PRT

<213> Homo sapiens

<210> 17
 <211> 924
 <212> DNA
 <213> Homo sapiens

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 ttgctgccct tggatatgat cctcattagc ttgggtgcct cccgcttctg cctgcagttg 180
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 agctggctca gtgtcctgtt ctgtgtgaag attgctaaca tcacacactc caccttcctg 360
 tggctgaagt ggaggttccc aggggtgggtg cctgggtcc tggtgggctc tgcctgatc 420
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<210> 18
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 18
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 Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
 20 25 30
 Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
 35 40 45
 Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
 50 55 60
 His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
 65 70 75 80
 Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
 85 90 95
 Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
 100 105 110
 Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Pro Gly
 115 120 125
 Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
 130 135 140

Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
145 150 155 160

Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
165 170 175

Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
180 185 190

Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
275 280 285

Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
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Trp Val Ala
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<210> 19

<211> 930

<212> DNA

<213> Homo sapiens

<400> 19

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gtttgtcatc tttttgtgat aaacatgaat cagattatat ggacaaaaga atatgaagga 480
aacatgactt ggaagatcaa actgaggagt gcaatgtacc tttcaaatac aacggtaacc 540
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atgaagggtcc acataaaagc tttgcaaact gtgacctcct tcctcttggt atgtgccatt 720
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<210> 20
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 20

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			20					25					30		
Ile	Glu	Trp	Phe	Lys	Arg	Gln	Lys	Ile	Ser	Phe	Ala	Asp	Gln	Ile	Leu
		35					40					45			
Thr	Ala	Leu	Ala	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Leu	Val	Leu
	50					55					60				
Asn	Trp	Tyr	Ala	Thr	Glu	Leu	Asn	Pro	Ala	Phe	Asn	Ser	Ile	Glu	Val
65					70					75					80
Arg	Ile	Thr	Ala	Tyr	Asn	Val	Trp	Ala	Val	Ile	Asn	His	Phe	Ser	Asn
				85					90					95	
Trp	Leu	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	Asn
			100					105					110		
Phe	Ser	Asn	Leu	Ile	Phe	Leu	His	Leu	Lys	Arg	Arg	Val	Lys	Ser	Val
		115					120					125			
Val	Leu	Val	Ile	Leu	Leu	Gly	Pro	Leu	Leu	Phe	Leu	Val	Cys	His	Leu
	130					135					140				
Phe	Val	Ile	Asn	Met	Asn	Gln	Ile	Ile	Trp	Thr	Lys	Glu	Tyr	Glu	Gly
145					150					155					160
Asn	Met	Thr	Trp	Lys	Ile	Lys	Leu	Arg	Ser	Ala	Met	Tyr	Leu	Ser	Asn
				165					170					175	
Thr	Thr	Val	Thr	Ile	Leu	Ala	Asn	Leu	Val	Pro	Phe	Thr	Leu	Thr	Leu
			180					185					190		
Ile	Ser	Phe	Leu	Leu	Leu	Ile	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys
		195					200					205			
Met	Gln	Leu	His	Gly	Lys	Gly	Ser	Gln	Asp	Pro	Ser	Met	Lys	Val	His
	210					215					220				
Ile	Lys	Ala	Leu	Gln	Thr	Val	Thr	Ser	Phe	Leu	Leu	Leu	Cys	Ala	Ile
225					230					235					240
Tyr	Phe	Leu	Ser	Ile	Ile	Met	Ser	Val	Trp	Ser	Phe	Glu	Ser	Leu	Glu
				245					250					255	
Asn	Lys	Pro	Val	Phe	Met	Phe	Cys	Glu	Ala	Ile	Ala	Phe	Ser	Tyr	Pro
			260					265					270		

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300

Lys Pro Ser Ser Ser
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<210> 21
 <211> 930
 <212> DNA
 <213> Homo sapiens

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 atctcctcag ctgaccaaact cctcactgct ctgggtggtct ccagaattgg tttactctgg 180
 gtcataattat tacattggta tgcaaatgtg ttttaattcag ctttatatag ttcagaagta 240
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 agcctcagca tattttatct gctcaagatt gccaatctct ccaaccttat tttctctcac 360
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 accaaggtcc acataaaagc tttgcaaact gtgatctcct tcctcatgtt atatgccatt 720
 tactttctgt atctaatac attaacctgg aatctttgaa cacagcagaa caaacttgta 780
 ttctgtcttt gccaaactct tggaatcatg tacccttcat tccactcatt cttcctgatt 840
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<210> 22
 <211> 885
 <212> DNA
 <213> Homo sapiens

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 atctcatcag ctgaccaaact ttctcactgc tctggtggtg tccagagttg gttactctg 180
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 aatttgtctt ggatgatcaa attgaggaat gcaatacagc tttcaaactt gactgtaacc 540
 atgccagcaa acgtcacacc ctgactctg acactaatat cttttctgct gttaatctat 600
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 accaaggtgc acataaaagc tttgcaaact gtgatctcct tccttatgtt atttgccatt 720
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<210> 23
 <211> 912
 <212> DNA
 <213> Mus sp.

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 acgttctctga tcctgcagac cctcttgatg tgcacagggc tgtccagact cggctctgcag 180
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 aaggaagagt ga 912

<210> 24
 <211> 303
 <212> PRT
 <213> Mus sp.

<400> 24
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 35 40 45
 Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
 50 55 60
 Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
 65 70 75 80
 Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
 85 90 95
 Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
 100 105 110
 Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
 115 120 125
 Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
 130 135 140

Thr	Ala	Thr	Val	Cys	Ile	Glu	Val	Gly	Phe	Pro	Leu	Ile	Glu	Asp	Gly
145					150					155					160
Tyr	Val	Leu	Arg	Asn	Ala	Gly	Leu	Asn	Asp	Ser	Asn	Ala	Lys	Leu	Val
				165					170					175	
Arg	Asn	Asn	Asp	Leu	Leu	Leu	Ile	Asn	Leu	Ile	Leu	Leu	Leu	Pro	Leu
			180					185					190		
Ser	Val	Phe	Val	Met	Cys	Thr	Ser	Met	Leu	Phe	Val	Ser	Leu	Tyr	Lys
		195					200					205			
His	Met	His	Trp	Met	Gln	Ser	Glu	Ser	His	Lys	Leu	Ser	Ser	Ala	Arg
	210					215					220				
Thr	Glu	Ala	His	Ile	Asn	Ala	Leu	Lys	Thr	Val	Thr	Thr	Phe	Phe	Cys
225					230					235					240
Phe	Phe	Val	Ser	Tyr	Phe	Ala	Ala	Phe	Met	Ala	Asn	Met	Thr	Phe	Arg
				245					250					255	
Ile	Pro	Tyr	Arg	Ser	His	Gln	Phe	Phe	Val	Val	Lys	Glu	Ile	Met	Ala
			260					265					270		
Ala	Tyr	Pro	Ala	Gly	His	Ser	Val	Ile	Ile	Val	Leu	Ser	Asn	Ser	Lys
		275					280					285			
Phe	Lys	Asp	Leu	Phe	Arg	Arg	Met	Ile	Cys	Leu	Gln	Lys	Glu	Glu	
	290					295					300				

<210> 25
 <211> 20
 <212> PRT
 <213> Artificial Sequence.

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 <223> Phe or Gly

<220>
 <221> MOD_RES
 <222> (3)
 <223> Ile, Val or Leu

<220>
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 <222> (4)
 <223> Val or Leu

<220>
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 <222> (6)
 <223> Ile or Val

<220>
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<222> (7)
 <223> Leu or Val

<220>
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 <222> (10)
 <223> Gly or Thr

<220>
 <221> MOD_RES
 <222> (13)
 <223> Val or Ala

<220>
 <221> MOD_RES
 <222> (18)
 <223> Ile or Met

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 25
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Cys Xaa Asp Trp
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<210> 26
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (1)
 <223> Asp or Gly

<220>
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 <223> Phe or Leu

<220>
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 <222> (3)
 <223> Ile or Leu

<220>
 <221> MOD_RES
 <222> (5)
 <223> Thr or Ile

<220>
 <221> MOD_RES

<222> (6)
 <223> Gly, Ala or Ser

<220>
 <221> MOD_RES
 <222> (13)
 <223> Cys, Gly or Phe

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 26
 Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
 1 5 10

<210> 27
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (3)
 <223> Leu or Phe

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ser, Thr or Asn

<220>
 <221> MOD_RES
 <222> (5)
 <223> Leu, Ile or Val

<220>
 <221> MOD_RES
 <222> (7)
 <223> Phe or Leu

<220>
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 <222> (8)
 <223> Ala or Thr

<220>
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 <222> (10)
 <223> Cys, Ser or Asn

<220>
 <221> MOD_RES
 <222> (12)
 <223> Ser, Asn or Gly

<220>
 <221> MOD_RES
 <222> (13)
 <223> Ile or Val

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 27
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 1 5 10

<210> 28
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> Phe or Cys

<220>
 <221> MOD_RES
 <222> (8)
 <223> Asn or Ser

<220>
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 <222> (11)
 <223> His or Asn

<220>
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 <222> (12)
 <223> Pro or Ser

<220>
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 <222> (13)
 <223> Leu, Ile or Val

<220>
 <221> MOD_RES
 <222> (16)
 <223> Trp or Tyr

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 28
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 1 5 10 15

Leu Lys

<210> 29
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (4)
 <223> Ile, Phe or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (10)
 <223> Ser or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (12)
 <223> Gln or Lys

<220>
 <221> MOD_RES
 <222> (13)
 <223> Met or Ile

<220>
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 <222> (14)
 <223> Gln or Lys

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 29
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 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ile or Val

<220>
 <221> MOD_RES
 <222> (7)
 <223> Leu or Met

<220>
 <221> MOD_RES
 <222> (8)
 <223> Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (10)
 <223> Pro, Ser or Asn

<220>
 <221> MOD_RES
 <222> (13)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (14)
 <223> Gln or Arg

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 30
 His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
 1 5 10

<210> 31
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide translocation domain

<400> 31
 Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys
 1 5 10 15

Thr Gly Val Val
 20